

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2004, 14:46:46 ; Search time 1 Seconds
(without alignments)
3.335 Million cell updates/sec

Title: us-09-919-162f-5

Perfect score: 776

Sequence: 1 tgaacagtcacacttgcaac.....gtccctgagaacaggatga 776

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 2149 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : us-09-728-911-1.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	755	97.3	2149	1	us-09-728-911-1

ALIGNMENTS

RESULT 1
us-09-728-911-1

Query Match		97.3%;	Score 755;	DB 1;	Length 2149;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 755;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	22	ATGATCCCTAAACATGCTTCTTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGATGCA	81		
DB	1	ATGATCCCTAAACATGCTTCTTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGATGCA	60		
QY	82	GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGTCACAAATTCAGTCCCGAAT	141		
DB	61	GGNACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGTCACAAATTCAGTCCCGAAT	120		
QY	142	TTTCACAACTTTTGCATGGCAGCTGGGAGGCACTTACTGGCAACAGCAGTGTCTAT	201		
DB	121	TTTCACAACTTTTGCATGGCAGCTGGGAGGCACTTACTGGCAACAGCAGTGTCTAT	180		
QY	202	TTTGTGCGATACAAATATATGACAGACANTGAAAAATAAAGAACTGTGGGCT	261		
DB	181	TTTGTGCGATACAAATATATGACAGACANTGAAAAATAAAGAACTGTGGGCT	240		
QY	262	ACTCAAGAACTCTCTTGTGACCTTACCAGTGAACCTCAGACATACAGGAACCTTATTAC	321		
DB	241	ACTCAAGAACTCTCTTGTGACCTTACCAGTGAACCTCAGACATACAGGAACCTTATTAC	300		

QY	322	GGGAGGTTGAGGGCGGCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCCGGTTTC	381		
DB	301	GGGAGGTTGAGGGCGGCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCCGGTTTC	360		
QY	382	ACTCCCTGGTGGGAAACAAAATAGATCCTCCAGTCATGAATATAACCCAGTCAATGGC	441		
DB	361	ACTCCCTGGTGGGAAACAAAATAGATCCTCCAGTCATGAATATAACCCAGTCAATGGC	420		
QY	442	TCTTTGTTGGTAATTCCTCCATGCTCCAAATTTACCATATAGATACCAAGGAAAAAAT	501		
DB	421	TCTTTGTTGGTAATTCCTCCATGCTCCAAATTTACCATATAGATACCAAGGAAAAAAT	480		
QY	502	GTATCTATAGAAGATTACTATGAACCTACTATACCGAGTTTCTTATTAATTAACAATCTACTA	561		
DB	481	GTATCTATAGAAGATTACTATGAACCTACTATACCGAGTTTCTTATTAATTAACAATCTACTA	540		
QY	562	GAAGAAGGACAAAAGGTTTATGAAGGGCTCACAGAGCGGTTGAAATTTGAAGCTCTAACA	621		
DB	541	GAAGAAGGACAAAAGGTTTATGAAGGGCTCACAGAGCGGTTGAAATTTGAAGCTCTAACA	600		
QY	622	CCACACTCCAGCTACTGTGTAGTGGCTGAAATATATCAGCCCATGTTTAGACAGAGAAGT	681		
DB	601	CCACACTCCAGCTACTGTGTAGTGGCTGAAATATATCAGCCCATGTTTAGACAGAGAAGT	660		
QY	682	CAGAGAGTGAAGAGAGATGTGGAAATCCATGCTTGTGGAAATTTGGCAATTCAGCAA	741		
DB	661	CAGAGAGTGAAGAGAGATGTGGAAATCCATGCTTGTGGAAATTTGGCAATTCAGCAA	720		
QY	742	TGTGGAATTTCAAAGCTCCCTGAGAACACAGGATGA	776		
DB	721	TGTGGAATTTCAAAGCTCCCTGAGAACACAGGATGA	755		

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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 17, 2004, 15:17:28 ; Search time 1.2 seconds
(without alignments)
0.993 Million cell updates/sec

Title: us-09-919-162f-6
Sequence: 1 MMPKHCFLGLISFPLTGVA.....YQPLDRRSQRSEERCVEIP 231

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 2149 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=soft -Qus-09-919-162f-6 -DB=us-09-728-911-1
-SUFFIX=ptc -OUT=09919162-6vs09728911-1.res -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdt -LIST=45
-DOALIGN=200 -THR_SCORE=ptc -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMF=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6
-NO_XLPXY -NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : us-09-728-911-1.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1244	100.0	2149	1	us-09-728-911-1

ALIGNMENTS

RESULT 1				
us-09-728-911-1				
Alignment Scores:				
Pred. No.:	0	Length:	2149	
Score:	1244.00	Matches:	231	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	1	Gaps:	0	
us-09-919-162f-6 (1-231) x us-09-728-911-1 (1-2149)				
Qy	1	MetMetProLysHisCysPheLeuGlyPheLeuIleSerPhePheLeuThrGlyValAla	20	